# Lars Bullinger

#### List of Publications by Citations

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67 306 148 22,571 h-index g-index citations papers 26,762 6.26 330 7.4 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
306	Genomic aberrations and survival in chronic lymphocytic leukemia. <i>New England Journal of Medicine</i> , <b>2000</b> , 343, 1910-6	59.2	2573
305	Genomic Classification and Prognosis in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , <b>2016</b> , 374, 2209-2221	59.2	1999
304	Mutations and treatment outcome in cytogenetically normal acute myeloid leukemia. <i>New England Journal of Medicine</i> , <b>2008</b> , 358, 1909-18	59.2	1330
303	Use of gene-expression profiling to identify prognostic subclasses in adult acute myeloid leukemia. <i>New England Journal of Medicine</i> , <b>2004</b> , 350, 1605-16	59.2	822
302	Mutant nucleophosmin (NPM1) predicts favorable prognosis in younger adults with acute myeloid leukemia and normal cytogenetics: interaction with other gene mutations. <i>Blood</i> , <b>2005</b> , 106, 3740-6	2.2	666
301	MLL-rearranged leukemia is dependent on aberrant H3K79 methylation by DOT1L. <i>Cancer Cell</i> , <b>2011</b> , 20, 66-78	24.3	647
300	V H mutation status, CD38 expression level, genomic aberrations, and survival in chronic lymphocytic leukemia. <i>Blood</i> , <b>2002</b> , 100, 1410-1416	2.2	633
299	IDH1 and IDH2 mutations are frequent genetic alterations in acute myeloid leukemia and confer adverse prognosis in cytogenetically normal acute myeloid leukemia with NPM1 mutation without FLT3 internal tandem duplication. <i>Journal of Clinical Oncology</i> , <b>2010</b> , 28, 3636-43	2.2	615
298	Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. <i>Cell</i> , <b>2012</b> , 148, 59-71	56.2	600
297	Lenalidomide induces ubiquitination and degradation of CK1lin del(5q) MDS. <i>Nature</i> , <b>2015</b> , 523, 183-18	850.4	468
296	Synthetic lethal interaction between oncogenic KRAS dependency and STK33 suppression in human cancer cells. <i>Cell</i> , <b>2009</b> , 137, 821-34	56.2	454
295	TP53 alterations in acute myeloid leukemia with complex karyotype correlate with specific copy number alterations, monosomal karyotype, and dismal outcome. <i>Blood</i> , <b>2012</b> , 119, 2114-21	2.2	411
294	A 17-gene stemness score for rapid determination of risk in acute leukaemia. <i>Nature</i> , <b>2016</b> , 540, 433-43	8 <b>7</b> 50.4	369
293	Gene mutations and treatment outcome in chronic lymphocytic leukemia: results from the CLL8 trial. <i>Blood</i> , <b>2014</b> , 123, 3247-54	2.2	352
292	MYC stimulates EZH2 expression by repression of its negative regulator miR-26a. <i>Blood</i> , <b>2008</b> , 112, 420	)2 <u>*</u> 12	333
291	Prognostic impact, concurrent genetic mutations, and gene expression features of AML with CEBPA mutations in a cohort of 1182 cytogenetically normal AML patients: further evidence for CEBPA double mutant AML as a distinctive disease entity. <i>Blood</i> , <b>2011</b> , 117, 2469-75	2.2	276
290	Differential impact of allelic ratio and insertion site in FLT3-ITD-positive AML with respect to allogeneic transplantation. <i>Blood</i> , <b>2014</b> , 124, 3441-9	2.2	260

## (2016-2017)

289	Genomics of Acute Myeloid Leukemia Diagnosis and Pathways. <i>Journal of Clinical Oncology</i> , <b>2017</b> , 35, 934-946	2.2	257
288	Musashi-2 regulates normal hematopoiesis and promotes aggressive myeloid leukemia. <i>Nature Medicine</i> , <b>2010</b> , 16, 903-8	50.5	252
287	RUNX1 mutations in acute myeloid leukemia: results from a comprehensive genetic and clinical analysis from the AML study group. <i>Journal of Clinical Oncology</i> , <b>2011</b> , 29, 1364-72	2.2	245
286	Distinct evolution and dynamics of epigenetic and genetic heterogeneity in acute myeloid leukemia. <i>Nature Medicine</i> , <b>2016</b> , 22, 792-9	50.5	217
285	Synergy between PI3K signaling and MYC in Burkitt lymphomagenesis. Cancer Cell, 2012, 22, 167-79	24.3	212
284	Lomustine-temozolomide combination therapy versus standard temozolomide therapy in patients with newly diagnosed glioblastoma with methylated MGMT promoter (CeTeG/NOA-09): a randomised, open-label, phase 3 trial. <i>Lancet, The</i> , <b>2019</b> , 393, 678-688	40	207
283	Clonal evolution in relapsed NPM1-mutated acute myeloid leukemia. <i>Blood</i> , <b>2013</b> , 122, 100-8	2.2	204
282	AKT/FOXO signaling enforces reversible differentiation blockade in myeloid leukemias. <i>Cell</i> , <b>2011</b> , 146, 697-708	56.2	203
281	Genetic and pharmacologic inhibition of I-catenin targets imatinib-resistant leukemia stem cells in CML. <i>Cell Stem Cell</i> , <b>2012</b> , 10, 412-24	18	185
280	Clonal evolution in chronic lymphocytic leukemia: acquisition of high-risk genomic aberrations associated with unmutated VH, resistance to therapy, and short survival. <i>Haematologica</i> , <b>2007</b> , 92, 1242	6.6 - <b>5</b>	179
279	TET2 mutations in acute myeloid leukemia (AML): results from a comprehensive genetic and clinical analysis of the AML study group. <i>Journal of Clinical Oncology</i> , <b>2012</b> , 30, 1350-7	2.2	166
278	Gene mutations and response to treatment with all-trans retinoic acid in elderly patients with acute myeloid leukemia. Results from the AMLSG Trial AML HD98B. <i>Haematologica</i> , <b>2009</b> , 94, 54-60	6.6	164
277	High-resolution genomic profiling of chronic lymphocytic leukemia reveals new recurrent genomic alterations. <i>Blood</i> , <b>2012</b> , 120, 4783-94	2.2	156
276	Expression of tumor-associated antigens in acute myeloid leukemia: Implications for specific immunotherapeutic approaches. <i>Blood</i> , <b>2006</b> , 108, 4109-17	2.2	156
275	Precision oncology for acute myeloid leukemia using a knowledge bank approach. <i>Nature Genetics</i> , <b>2017</b> , 49, 332-340	36.3	155
274	PI3 Kinase and FOXO1 Transcription Factor Activity Differentially Control B Cells in the Germinal Center Light and Dark Zones. <i>Immunity</i> , <b>2015</b> , 43, 1075-86	32.3	155
273	BCAT1 restricts <b>K</b> G levels in AML stem cells leading to IDHmut-like DNA hypermethylation. <i>Nature</i> , <b>2017</b> , 551, 384-388	50.4	154
272	The genomic landscape of core-binding factor acute myeloid leukemias. <i>Nature Genetics</i> , <b>2016</b> , 48, 1551	-36.56	147

271	Prognostic impact of WT1 mutations in cytogenetically normal acute myeloid leukemia: a study of the German-Austrian AML Study Group. <i>Blood</i> , <b>2009</b> , 113, 4505-11	2.2	142
270	Measurable residual disease monitoring by NGS before allogeneic hematopoietic cell transplantation in AML. <i>Blood</i> , <b>2018</b> , 132, 1703-1713	2.2	142
269	Secondary genetic lesions in acute myeloid leukemia with inv(16) or t(16;16): a study of the German-Austrian AML Study Group (AMLSG). <i>Blood</i> , <b>2013</b> , 121, 170-7	2.2	134
268	Clinical impact of DNMT3A mutations in younger adult patients with acute myeloid leukemia: results of the AML Study Group (AMLSG). <i>Blood</i> , <b>2013</b> , 121, 4769-77	2.2	129
267	Up-regulation of a HOXA-PBX3 homeobox-gene signature following down-regulation of miR-181 is associated with adverse prognosis in patients with cytogenetically abnormal AML. <i>Blood</i> , <b>2012</b> , 119, 23	1 <del>2:2</del> 4	128
266	Disclosure of candidate genes in acute myeloid leukemia with complex karyotypes using microarray-based molecular characterization. <i>Journal of Clinical Oncology</i> , <b>2006</b> , 24, 3887-94	2.2	127
265	Quantitative DNA methylation predicts survival in adult acute myeloid leukemia. <i>Blood</i> , <b>2010</b> , 115, 636-	<b>42</b> .2	121
264	Differential niche and Wnt requirements during acute myeloid leukemia progression. <i>Blood</i> , <b>2011</b> , 118, 2849-56	2.2	118
263	The value of allogeneic and autologous hematopoietic stem cell transplantation in prognostically favorable acute myeloid leukemia with double mutant CEBPA. <i>Blood</i> , <b>2013</b> , 122, 1576-82	2.2	115
262	Identification of a 24-gene prognostic signature that improves the European LeukemiaNet risk classification of acute myeloid leukemia: an international collaborative study. <i>Journal of Clinical Oncology</i> , <b>2013</b> , 31, 1172-81	2.2	112
261	t(11;14)-positive mantle cell lymphomas exhibit complex karyotypes and share similarities with B-cell chronic lymphocytic leukemia <b>2000</b> , 27, 285-294		112
260	Commonly altered genomic regions in acute myeloid leukemia are enriched for somatic mutations involved in chromatin remodeling and splicing. <i>Blood</i> , <b>2012</b> , 120, e83-92	2.2	110
259	Prognostic impact of minimal residual disease in CBFB-MYH11-positive acute myeloid leukemia. Journal of Clinical Oncology, <b>2010</b> , 28, 3724-9	2.2	110
258	Disease evolution and outcomes in familial AML with germline CEBPA mutations. <i>Blood</i> , <b>2015</b> , 126, 121	4 <u>223</u> 3	104
257	Gene-expression profiling identifies distinct subclasses of core binding factor acute myeloid leukemia. <i>Blood</i> , <b>2007</b> , 110, 1291-300	2.2	100
256	The homeobox gene CDX2 is aberrantly expressed in most cases of acute myeloid leukemia and promotes leukemogenesis. <i>Journal of Clinical Investigation</i> , <b>2007</b> , 117, 1037-48	15.9	100
255	Role of Donor Clonal Hematopoiesis in Allogeneic Hematopoietic Stem-Cell Transplantation. Journal of Clinical Oncology, <b>2019</b> , 37, 375-385	2.2	97
254	PBX3 is an important cofactor of HOXA9 in leukemogenesis. <i>Blood</i> , <b>2013</b> , 121, 1422-31	2.2	93

## (2014-2010)

253	Modulation of calcium-activated potassium channels induces cardiogenesis of pluripotent stem cells and enrichment of pacemaker-like cells. <i>Circulation</i> , <b>2010</b> , 122, 1823-36	16.7	89
252	Gene expression profiling in acute myeloid leukemia. <i>Journal of Clinical Oncology</i> , <b>2005</b> , 23, 6296-305	2.2	84
251	Low-grade Glioma Surgery in Intraoperative Magnetic Resonance Imaging: Results of a Multicenter Retrospective Assessment of the German Study Group for Intraoperative Magnetic Resonance Imaging. <i>Neurosurgery</i> , <b>2016</b> , 78, 775-86	3.2	83
250	An FLT3 gene-expression signature predicts clinical outcome in normal karyotype AML. <i>Blood</i> , <b>2008</b> , 111, 4490-5	2.2	83
249	Comparing cancer vs normal gene expression profiles identifies new disease entities and common transcriptional programs in AML patients. <i>Blood</i> , <b>2014</b> , 123, 894-904	2.2	82
248	Venetoclax resistance and acquired mutations in chronic lymphocytic leukemia. <i>Haematologica</i> , <b>2019</b> , 104, e434-e437	6.6	81
247	Comprehensive analysis of mammalian miRNA* species and their role in myeloid cells. <i>Blood</i> , <b>2011</b> , 118, 3350-8	2.2	81
246	Neutrophil development and function critically depend on Bruton tyrosine kinase in a mouse model of X-linked agammaglobulinemia. <i>Blood</i> , <b>2011</b> , 117, 1329-39	2.2	81
245	Leukemia-associated antigens are critical for the proliferation of acute myeloid leukemia cells. <i>Clinical Cancer Research</i> , <b>2008</b> , 14, 7161-6	12.9	78
244	QOLP-20. QUALITY OF LIFE IN THE PHASE III CeTeG/NOA-09 TRIAL RANDOMIZING CCNU/TEMOZOLOMIDE (TMZ) COMBINATION THERAPY VS. STANDARD TMZ THERAPY FOR NEWLY DIAGNOSED MGMT-METHYLATED GLIOBLASTOMA. <i>Neuro-Oncology</i> , <b>2018</b> , 20, vi218-vi219	1	78
243	Hematopoietic lineage distribution and evolutionary dynamics of clonal hematopoiesis. <i>Leukemia</i> , <b>2018</b> , 32, 1908-1919	10.7	75
242	UTX-mediated enhancer and chromatin remodeling suppresses myeloid leukemogenesis through noncatalytic inverse regulation of ETS and GATA programs. <i>Nature Genetics</i> , <b>2018</b> , 50, 883-894	36.3	73
241	SIRT1 prevents genotoxic stress-induced p53 activation in acute myeloid leukemia. <i>Blood</i> , <b>2014</b> , 124, 121-33	2.2	70
240	ASXL1 mutations in younger adult patients with acute myeloid leukemia: a study by the German-Austrian Acute Myeloid Leukemia Study Group. <i>Haematologica</i> , <b>2015</b> , 100, 324-30	6.6	67
239	Clonal evolution patterns in acute myeloid leukemia with NPM1 mutation. <i>Nature Communications</i> , <b>2019</b> , 10, 2031	17.4	63
238	Therapeutic targeting of preleukemia cells in a mouse model of mutant acute myeloid leukemia. <i>Science</i> , <b>2020</b> , 367, 586-590	33.3	63
237	Cytogenetics and gene mutations influence survival in older patients with acute myeloid leukemia treated with azacitidine or conventional care. <i>Leukemia</i> , <b>2018</b> , 32, 2546-2557	10.7	62
236	Differential methylation in CN-AML preferentially targets non-CGI regions and is dictated by DNMT3A mutational status and associated with predominant hypomethylation of HOX genes. <i>Epigenetics</i> , <b>2014</b> , 9, 1108-19	5.7	61

235	Genomic landscape and clonal evolution of acute myeloid leukemia with t(8;21): an international study on 331 patients. <i>Blood</i> , <b>2019</b> , 133, 1140-1151	2.2	61
234	Contrasting requirements during disease evolution identify EZH2 as a therapeutic target in AML. <i>Journal of Experimental Medicine</i> , <b>2019</b> , 216, 966-981	16.6	60
233	SCFFbxo9 and CK2 direct the cellular response to growth factor withdrawal via Tel2/Tti1 degradation and promote survival in multiple myeloma. <i>Nature Cell Biology</i> , <b>2013</b> , 15, 72-81	23.4	60
232	High-resolution genomic profiling of adult and pediatric core-binding factor acute myeloid leukemia reveals new recurrent genomic alterations. <i>Blood</i> , <b>2012</b> , 119, e67-75	2.2	59
231	High expression of lymphoid enhancer-binding factor-1 (LEF1) is a novel favorable prognostic factor in cytogenetically normal acute myeloid leukemia. <i>Blood</i> , <b>2012</b> , 120, 2118-26	2.2	59
230	Gene-expression profiles and their association with drug resistance in adult acute myeloid leukemia. <i>Haematologica</i> , <b>2005</b> , 90, 1484-92	6.6	59
229	Telomerase inhibition effectively targets mouse and human AML stem cells and delays relapse following chemotherapy. <i>Cell Stem Cell</i> , <b>2014</b> , 15, 775-90	18	56
228	New Targeted Agents in Acute Myeloid Leukemia: New Hope on the Rise. <i>International Journal of Molecular Sciences</i> , <b>2019</b> , 20,	6.3	54
227	Adding dasatinib to intensive treatment in core-binding factor acute myeloid leukemia-results of the AMLSG 11-08 trial. <i>Leukemia</i> , <b>2018</b> , 32, 1621-1630	10.7	53
226	Circular RNAs of the nucleophosmin (NPM1) gene in acute myeloid leukemia. <i>Haematologica</i> , <b>2017</b> , 102, 2039-2047	6.6	51
225	MYC-containing amplicons in acute myeloid leukemia: genomic structures, evolution, and transcriptional consequences. <i>Leukemia</i> , <b>2018</b> , 32, 2152-2166	10.7	50
224	Early hematopoietic zinc finger protein-zinc finger protein 521: a candidate regulator of diverse immature cells. <i>International Journal of Biochemistry and Cell Biology</i> , <b>2008</b> , 40, 848-54	5.6	50
223	Gene expression and mutation-guided synthetic lethality eradicates proliferating and quiescent leukemia cells. <i>Journal of Clinical Investigation</i> , <b>2017</b> , 127, 2392-2406	15.9	49
222	Epigenetic therapy: azacytidine and decitabine in acute myeloid leukemia. <i>Expert Review of Hematology</i> , <b>2018</b> , 11, 361-371	2.8	46
221	Measurable residual disease monitoring in acute myeloid leukemia with t(8;21)(q22;q22.1): results from the AML Study Group. <i>Blood</i> , <b>2019</b> , 134, 1608-1618	2.2	45
220	Prognostic and predictive impact of genetic markers in patients with CLL treated with obinutuzumab and venetoclax. <i>Blood</i> , <b>2020</b> , 135, 2402-2412	2.2	43
219	Common and overlapping oncogenic pathways contribute to the evolution of acute myeloid leukemias. <i>Cancer Research</i> , <b>2011</b> , 71, 4117-29	10.1	42
218	The cell fate determinant Llgl1 influences HSC fitness and prognosis in AML. <i>Journal of Experimental Medicine</i> , <b>2013</b> , 210, 15-22	16.6	40

## (2020-2010)

217	High-resolution single-nucleotide polymorphism array-profiling in myeloproliferative neoplasms identifies novel genomic aberrations. <i>Haematologica</i> , <b>2010</b> , 95, 666-9	6.6	40
216	Identification of gene expression-based prognostic markers in the hematopoietic stem cells of patients with myelodysplastic syndromes. <i>Journal of Clinical Oncology</i> , <b>2013</b> , 31, 3557-64	2.2	39
215	Id1 is a common downstream target of oncogenic tyrosine kinases in leukemic cells. <i>Blood</i> , <b>2008</b> , 112, 1981-92	2.2	39
214	CDX2-driven leukemogenesis involves KLF4 repression and deregulated PPARIsignaling. <i>Journal of Clinical Investigation</i> , <b>2013</b> , 123, 299-314	15.9	38
213	Tyrosine kinase inhibitor-induced defects in DNA repair sensitize FLT3(ITD)-positive leukemia cells to PARP1 inhibitors. <i>Blood</i> , <b>2018</b> , 132, 67-77	2.2	38
212	The VEGF receptor, neuropilin-1, represents a promising novel target for chronic lymphocytic leukemia patients. <i>International Journal of Cancer</i> , <b>2013</b> , 133, 1489-96	7.5	37
211	Delineation of distinct tumour profiles in mantle cell lymphoma by detailed cytogenetic, interphase genetic and morphological analysis. <i>British Journal of Haematology</i> , <b>2008</b> , 142, 538-50	4.5	37
<b>21</b> 0	Genomic aberrations in mantle cell lymphoma detected by interphase fluorescence in situ hybridization. Incidence and clinicopathological correlations. <i>Haematologica</i> , <b>2008</b> , 93, 680-7	6.6	37
209	Jak2V617F and Dnmt3a loss cooperate to induce myelofibrosis through activated enhancer-driven inflammation. <i>Blood</i> , <b>2018</b> , 132, 2707-2721	2.2	37
208	Targeted sequencing using a 47 gene multiple myeloma mutation panel (M(3) P) in -17p high risk disease. <i>British Journal of Haematology</i> , <b>2015</b> , 168, 507-10	4.5	36
207	Integrative nucleophosmin mutation-associated microRNA and gene expression pattern analysis identifies novel microRNA - target gene interactions in acute myeloid leukemia. <i>Haematologica</i> , <b>2011</b> , 96, 1783-91	6.6	36
206	KIT mutations confer a distinct gene expression signature in core binding factor leukaemia. <i>British Journal of Haematology</i> , <b>2010</b> , 148, 925-37	4.5	36
205	SEURAT: visual analytics for the integrated analysis of microarray data. <i>BMC Medical Genomics</i> , <b>2010</b> , 3, 21	3.7	35
204	Repressing the repressor: a new mode of MYC action in lymphomagenesis. <i>Cell Cycle</i> , <b>2009</b> , 8, 556-9	4.7	34
203	Expression profiling of leukemia patients: key lessons and future directions. <i>Experimental Hematology</i> , <b>2014</b> , 42, 651-60	3.1	33
202	Aneuploid acute myeloid leukemia exhibits a signature of genomic alterations in the cell cycle and protein degradation machinery. <i>Cancer</i> , <b>2019</b> , 125, 712-725	6.4	33
201	Targeting components of the alternative NHEJ pathway sensitizes KRAS mutant leukemic cells to chemotherapy. <i>Blood</i> , <b>2014</b> , 123, 2355-66	2.2	32
<b>2</b> 00	Aldehyde dehydrogenase 3a2 protects AML cells from oxidative death and the synthetic lethality of ferroptosis inducers. <i>Blood</i> , <b>2020</b> , 136, 1303-1316	2.2	31

199	Chromothripsis is linked to alteration, cell cycle impairment, and dismal outcome in acute myeloid leukemia with complex karyotype. <i>Haematologica</i> , <b>2018</b> , 103, e17-e20	6.6	31
198	Impact of gemtuzumab ozogamicin on MRD and relapse risk in patients with NPM1-mutated AML: results from the AMLSG 09-09 trial. <i>Blood</i> , <b>2020</b> , 136, 3041-3050	2.2	30
197	PRAME-induced inhibition of retinoic acid receptor signaling-mediated differentiationa possible target for ATRA response in AML without t(15;17). <i>Clinical Cancer Research</i> , <b>2013</b> , 19, 2562-71	12.9	29
196	Circular RNAs in Cancer. Advances in Experimental Medicine and Biology, 2018, 1087, 215-230	3.6	29
195	HOXA/PBX3 knockdown impairs growth and sensitizes cytogenetically normal acute myeloid leukemia cells to chemotherapy. <i>Haematologica</i> , <b>2013</b> , 98, 1216-25	6.6	27
194	Quantitative comparison of microarray experiments with published leukemia related gene expression signatures. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 422	3.6	27
193	GP130 activation induces myeloma and collaborates with MYC. <i>Journal of Clinical Investigation</i> , <b>2014</b> , 124, 5263-74	15.9	27
192	Gene expression with prognostic implications in cytogenetically normal acute myeloid leukemia. <i>Seminars in Oncology</i> , <b>2008</b> , 35, 356-64	5.5	26
191	Nuclear FOXO1 promotes lymphomagenesis in germinal center B cells. <i>Blood</i> , <b>2018</b> , 132, 2670-2683	2.2	26
190	IGF1R as druggable target mediating PI3K-linhibitor resistance in a murine model of chronic lymphocytic leukemia. <i>Blood</i> , <b>2019</b> , 134, 534-547	2.2	25
189	Early aberrant DNA methylation events in a mouse model of acute myeloid leukemia. <i>Genome Medicine</i> , <b>2014</b> , 6, 34	14.4	25
188	High BRE expression predicts favorable outcome in adult acute myeloid leukemia, in particular among MLL-AF9-positive patients. <i>Blood</i> , <b>2011</b> , 118, 5613-21	2.2	25
187	Cancer-specific changes in DNA methylation reveal aberrant silencing and activation of enhancers in leukemia. <i>Blood</i> , <b>2017</b> , 129, e13-e25	2.2	24
186	Splicing factor YBX1 mediates persistence of JAK2-mutated neoplasms. <i>Nature</i> , <b>2020</b> , 588, 157-163	50.4	24
185	Single-cell analysis based dissection of clonality in myelofibrosis. <i>Nature Communications</i> , <b>2020</b> , 11, 73	17.4	23
184	Quantitative proteomics reveals specific metabolic features of acute myeloid leukemia stem cells. <i>Blood</i> , <b>2020</b> , 136, 1507-1519	2.2	22
183	Clonal hematopoiesis in patients with anti-neutrophil cytoplasmic antibody-associated vasculitis. Haematologica, <b>2020</b> , 105, e264-e267	6.6	22
182	Impact of MLL5 expression on decitabine efficacy and DNA methylation in acute myeloid leukemia. Haematologica, <b>2014</b> , 99, 1456-64	6.6	22

181	Partitioned learning of deep Boltzmann machines for SNP data. <i>Bioinformatics</i> , <b>2017</b> , 33, 3173-3180	7.2	22
180	getITD for FLT3-ITD-based MRD monitoring in AML. <i>Leukemia</i> , <b>2019</b> , 33, 2535-2539	10.7	20
179	NCAM1 (CD56) promotes leukemogenesis and confers drug resistance in AML. <i>Blood</i> , <b>2019</b> , 133, 2305-2	1319	20
178	Functional Classification of Mutations in Acute Myeloid Leukemia. <i>Cancers</i> , <b>2020</b> , 12,	6.6	20
177	HELP for AML: methylation profiling opens new avenues. <i>Cancer Cell</i> , <b>2010</b> , 17, 1-3	24.3	20
176	Acute myeloid leukemia with mutated nucleophosmin 1: an immunogenic acute myeloid leukemia subtype and potential candidate for immune checkpoint inhibition. <i>Haematologica</i> , <b>2017</b> , 102, e499-e50	6.6	19
175	Clonal evolution of acute myeloid leukemia with FLT3-ITD mutation under treatment with midostaurin. <i>Blood</i> , <b>2021</b> , 137, 3093-3104	2.2	19
174	Molecular dissection of valproic acid effects in acute myeloid leukemia identifies predictive networks. <i>Epigenetics</i> , <b>2016</b> , 11, 517-25	5.7	18
173	CXXC5 (retinoid-inducible nuclear factor, RINF) is a potential therapeutic target in high-risk human acute myeloid leukemia. <i>Oncotarget</i> , <b>2013</b> , 4, 1438-48	3.3	18
172	The patientsQiew: impact of the extent of resection, intraoperative imaging, and awake surgery on health-related quality of life in high-grade glioma patients-results of a multicenter cross-sectional study. <i>Neurosurgical Review</i> , <b>2018</b> , 41, 207-219	3.9	17
171	Haploinsufficiency of ETV6 and CDKN1B in patients with acute myeloid leukemia and complex karyotype. <i>BMC Genomics</i> , <b>2014</b> , 15, 784	4.5	17
170	Evaluating the impact of genetic and epigenetic aberrations on survival and response in acute myeloid leukemia patients receiving epigenetic therapy. <i>Annals of Hematology</i> , <b>2017</b> , 96, 559-565	3	16
169	Health-related quality of life and neurocognitive functioning with lomustine-temozolomide versus temozolomide in patients with newly diagnosed, MGMT-methylated glioblastoma (CeTeG/NOA-09): a randomised, multicentre, open-label, phase 3 trial. <i>Lancet Oncology, The</i> , <b>2019</b> , 20, 1444-1453	21.7	16
168	DNA methylation profiling in acute myeloid leukemia: from recent technological advances to biological and clinical insights. <i>Future Oncology</i> , <b>2010</b> , 6, 1415-31	3.6	15
167	BCMSUN, a candidate gene for B-cell chronic lymphocytic leukemia and mantle-cell lymphoma, has an independently expressed homolog on 1p22-p31, BCMSUN-like. <i>International Journal of Cancer</i> , <b>2000</b> , 88, 692-7	7.5	15
166	Identifying ischemic stroke associated with cancer: a multiple model derived from a case-control analysis. <i>Journal of Neurology</i> , <b>2017</b> , 264, 781-791	5.5	14
165	Prognostic and predictive role of gene mutations in chronic lymphocytic leukemia: results from the pivotal phase III study COMPLEMENT1. <i>Haematologica</i> , <b>2020</b> , 105, 2440-2447	6.6	14
164	Array-based cytogenetic approaches in acute myeloid leukemia: clinical impact and biological insights. <i>Seminars in Oncology</i> , <b>2012</b> , 39, 37-46	5.5	14

163	Targeting inhibitor of apoptosis proteins by Smac mimetic elicits cell death in poor prognostic subgroups of chronic lymphocytic leukemia. <i>International Journal of Cancer</i> , <b>2015</b> , 137, 2959-70	7.5	14
162	Leukemic progenitor cells are susceptible to targeting by stimulated cytotoxic T cells against immunogenic leukemia-associated antigens. <i>International Journal of Cancer</i> , <b>2015</b> , 137, 2083-92	7.5	14
161	SSX2IP expression in acute myeloid leukaemia: an association with mitotic spindle failure in t(8;21), and cell cycle in t(15;17) patients. <i>British Journal of Haematology</i> , <b>2008</b> , 140, 250-1	4.5	14
160	Localization-associated immune phenotypes of clonally expanded tumor-infiltrating T cells and distribution of their target antigens in rectal cancer. <i>OncoImmunology</i> , <b>2019</b> , 8, e1586409	7.2	13
159	MicroRNA-155 is upregulated in MLL-rearranged AML but its absence does not affect leukemia development. <i>Experimental Hematology</i> , <b>2016</b> , 44, 1166-1171	3.1	13
158	Mutant CEBPA directly drives the expression of the targetable tumor-promoting factor CD73 in AML. <i>Science Advances</i> , <b>2019</b> , 5, eaaw4304	14.3	13
157	ACTR-58. PHASE III TRIAL OF CCNU/TEMOZOLOMIDE (TMZ) COMBINATION THERAPY VS. STANDARD TMZ THERAPY FOR NEWLY DIAGNOSED MGMT-METHYLATED GLIOBLASTOMA PATIENTS: THE CeTeg/NOA-09 trial. <i>Neuro-Oncology</i> , <b>2017</b> , 19, vi13-vi14	1	13
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154	The cell fate determinant Scribble is required for maintenance of hematopoietic stem cell function. <i>Leukemia</i> , <b>2018</b> , 32, 1211-1221	10.7	11
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152	FACS single cell index sorting is highly reliable and determines immune phenotypes of clonally expanded TItells. <i>European Journal of Immunology</i> , <b>2018</b> , 48, 1248-1250	6.1	11
151	Genomic heterogeneity in core-binding factor acute myeloid leukemia and its clinical implication. <i>Blood Advances</i> , <b>2020</b> , 4, 6342-6352	7.8	11
150	Predicting sinusoidal obstruction syndrome after allogeneic stem cell transplantation with the EASIX biomarker panel. <i>Haematologica</i> , <b>2021</b> , 106, 446-453	6.6	11
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148	Altered NFE2 activity predisposes to leukemic transformation and myelosarcoma with AML-specific aberrations. <i>Blood</i> , <b>2019</b> , 133, 1766-1777	2.2	10
147	Monosomal karyotype and chromosome 17p loss or TP53 mutations in decitabine-treated patients with acute myeloid leukemia. <i>Annals of Hematology</i> , <b>2020</b> , 99, 1551-1560	3	10
146	Genome-wide genotyping of acute myeloid leukemia with translocation t(9;11)(p22;q23) reveals novel recurrent genomic alterations. <i>Haematologica</i> , <b>2014</b> , 99, e133-5	6.6	10

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144	Gene Mutations as Predicitive Markers for Postremission Therapy in Younger Adults with Normal Karyotype AML <i>Blood</i> , <b>2006</b> , 108, 4-4	2.2	10
143	Smac mimetic induces cell death in a large proportion of primary acute myeloid leukemia samples, which correlates with defined molecular markers. <i>Oncotarget</i> , <b>2016</b> , 7, 49539-49551	3.3	10
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141	Prospective identification of resistance mechanisms to HSP90 inhibition in KRAS mutant cancer cells. <i>Oncotarget</i> , <b>2017</b> , 8, 7678-7690	3.3	9
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134	A Randomized Open label Phase-II Clinical Trial with or without Infusion of Plasma from Subjects after Convalescence of SARS-CoV-2 Infection in High-Risk Patients with Confirmed Severe SARS-CoV-2 Disease (RECOVER): A structured summary of a study protocol for a randomised	2.8	7
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118	Precision medicine in myeloid malignancies. <i>Seminars in Cancer Biology</i> , <b>2021</b> ,  Micro-ribonucleic acid-155 is a direct target of Meis1, but not a driver in acute myeloid leukemia. <i>Haematologica</i> , <b>2018</b> , 103, 246-255	12.7 6.6	5
	Micro-ribonucleic acid-155 is a direct target of Meis1, but not a driver in acute myeloid leukemia.		
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117	Micro-ribonucleic acid-155 is a direct target of Meis1, but not a driver in acute myeloid leukemia. Haematologica, 2018, 103, 246-255  Gene expression analysis of decitabine treated AML: high impact of tumor suppressor gene expression changes. Leukemia and Lymphoma, 2017, 58, 1-4  Specific T-cell immune responses against colony-forming cells including leukemic progenitor cells of AML patients were increased by immune checkpoint inhibition. Cancer Immunology,	6.6	5
117 116 115	Micro-ribonucleic acid-155 is a direct target of Meis1, but not a driver in acute myeloid leukemia. Haematologica, 2018, 103, 246-255  Gene expression analysis of decitabine treated AML: high impact of tumor suppressor gene expression changes. Leukemia and Lymphoma, 2017, 58, 1-4  Specific T-cell immune responses against colony-forming cells including leukemic progenitor cells of AML patients were increased by immune checkpoint inhibition. Cancer Immunology, Immunotherapy, 2020, 69, 629-640	6.6 1.9 7.4	5
117 116 115	Micro-ribonucleic acid-155 is a direct target of Meis1, but not a driver in acute myeloid leukemia. Haematologica, 2018, 103, 246-255  Gene expression analysis of decitabine treated AML: high impact of tumor suppressor gene expression changes. Leukemia and Lymphoma, 2017, 58, 1-4  Specific T-cell immune responses against colony-forming cells including leukemic progenitor cells of AML patients were increased by immune checkpoint inhibition. Cancer Immunology, Immunotherapy, 2020, 69, 629-640  GiANT: gene set uncertainty in enrichment analysis. Bioinformatics, 2016, 32, 1891-4  Detection of mutant NPM1 mRNA in acute myeloid leukemia using custom gene expression arrays.	6.6 1.9 7.4	5 4 4
117 116 115 114	Micro-ribonucleic acid-155 is a direct target of Meis1, but not a driver in acute myeloid leukemia. Haematologica, 2018, 103, 246-255  Gene expression analysis of decitabine treated AML: high impact of tumor suppressor gene expression changes. Leukemia and Lymphoma, 2017, 58, 1-4  Specific T-cell immune responses against colony-forming cells including leukemic progenitor cells of AML patients were increased by immune checkpoint inhibition. Cancer Immunology, Immunotherapy, 2020, 69, 629-640  GiANT: gene set uncertainty in enrichment analysis. Bioinformatics, 2016, 32, 1891-4  Detection of mutant NPM1 mRNA in acute myeloid leukemia using custom gene expression arrays. Genetic Testing and Molecular Biomarkers, 2013, 17, 295-300  VENTX induces expansion of primitive erythroid cells and contributes to the development of acute	6.6 1.9 7.4 7.2	5 4 4

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107	Molecular landscape and prognostic impact of FLT3-ITD insertion site in acute myeloid leukemia: RATIFY study results. <i>Leukemia</i> , <b>2021</b> ,	10.7	4
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95	Integration of Hi-C and Nanopore Sequencing for Structural Variant Analysis in AML with a Complex Karyotype: (Chromothripsis) [Image: Blood, <b>2020</b> , 136, 28-28	2.2	2
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86	MYC-containing amplicons in acute myeloid leukemia: genomic structures, evolution, and transcriptional consequences. <i>Leukemia</i> , <b>2017</b> ,	10.7	1
85	Functional Classification of TP53 Mutations in Acute Myeloid Leukemia. <i>Blood</i> , <b>2019</b> , 134, 2725-2725	2.2	1
84	Characterization of NPM1-Mutated/FLT3 ITD-Negative Acute Myeloid Leukemia with Normal Karyotype by Gene Expression Profiling <i>Blood</i> , <b>2006</b> , 108, 155-155	2.2	1
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82	Thalidomide Alone and in Combination with Fludarabine Exerts Distinct Molecular and Antileukemic Effects in B-Cell Chronic Lymphocytic Leukemia <i>Blood</i> , <b>2007</b> , 110, 3124-3124	2.2	1
81	Combined Analysis of Valproic Acid Induced MicroRNA and Gene Expression Changes in Acute Myeloid Leukemia <i>Blood</i> , <b>2007</b> , 110, 869-869	2.2	1
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79	MYB induces the expression of the oncogenic corepressor SKI in acute myeloid leukemia. <i>Oncotarget</i> , <b>2018</b> , 9, 22423-22435	3.3	1
78	CTNI-04. RECURRENT GLIOBLASTOMA LONG-TERM SURVIVORS TREATED WITH CUSP9v3. <i>Neuro-Oncology</i> , <b>2021</b> , 23, vi59-vi59	1	1
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76	Array-CGH and Gene Expression Profiling Based Molecular Characterization of Myeloid Leukemia Cell Lines <i>Blood</i> , <b>2005</b> , 106, 4397-4397	2.2	1
75	Genomics in Leukemias <b>2009</b> , 844-855		1
74	Partitioned Learning of Deep Boltzmann Machines for SNP Data		1

73	Efficiency of Leukemic Stem Cell Separation From Patients with Acute Myeloid Leukemia. <i>Blood</i> , <b>2011</b> , 118, 4997-4997	2.2	1
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69	Netboost: Boosting-Supported Network Analysis Improves High-Dimensional Omics Prediction in Acute Myeloid Leukemia and Huntington@ Disease. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 2635-2648	3	1
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65	Application of precision medicine in clinical routine in haematology@hallenges and opportunities. Journal of Internal Medicine,	10.8	1
64	Acute left ventricular insufficiency in a Burkitt Lymphoma patient with myocardial involvement and extensive local tumor cell lysis: a case report <i>BMC Cardiovascular Disorders</i> , <b>2022</b> , 22, 31	2.3	О
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58	EASIX and Severe Endothelial Complications After CD19-Directed CAR-T Cell Therapy-A Cohort Study <i>Frontiers in Immunology</i> , <b>2022</b> , 13, 877477	8.4	O
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52	Targeting Control of Cell Cycle Enhances the Activity of Conventional Chemotherapy in Chemotherapy-Resistant Acute Myeloid Leukemia. <i>Blood</i> , <b>2021</b> , 138, 2241-2241	2.2
51	Flow Cytometric Analysis of Microbial Diversity in Patients with Aggressive Lymphoma Disease Undergoing Chemoimmunotherapy. <i>Blood</i> , <b>2021</b> , 138, 4005-4005	2.2
50	The CAR-Hematotox Identifies Patients at High Risk for Prolonged Neutropenia, Infectious Complications and Prolonged Hospitalization Following CD19-CART in R/R LBCL. <i>Blood</i> , <b>2021</b> , 138, 385	2- <del>3</del> 852
49	Drug-Response Signature Predicts Outcome in Adult Acute Myeloid Leukemia and Associates Poor Response with Molecular Characteristics of Hematopoietic Stem Cells <i>Blood</i> , <b>2004</b> , 104, 2024-2024	2.2
48	Identification of Distinct inv(16) Subclasses in Adult Acute Myeloid Leukemia Based on Gene Expression Profiling <i>Blood</i> , <b>2004</b> , 104, 2037-2037	2.2
47	Prognostic Gene-Expression Signatures in Adult Acute Myeloid Leukemia with Normal Karyotype <i>Blood</i> , <b>2005</b> , 106, 756-756	2.2
46	Gene Expression Profiling Identifies Distinct Subclasses in Core Binding Factor Acute Myeloid Leukemia <i>Blood</i> , <b>2005</b> , 106, 673-673	2.2
45	A FLT3 Gene-Expression Signature Outperforms FLT3 Status in Predicting Clinical Outcome for Patients with Normal Karyotype AML <i>Blood</i> , <b>2006</b> , 108, 2311-2311	2.2
44	Identification of High-Level DNA Amplifications in AML with Complex Karyotype Using Array-CGH <i>Blood</i> , <b>2006</b> , 108, 1914-1914	2.2
43	Expression of Tumor-Associated Antigens (TAAs) in Acute Myeloid Leukemia (AML) Correlated with Specific T Cell Responses and Survival <i>Blood</i> , <b>2006</b> , 108, 414-414	2.2
42	In Vitro and In Vivo Monitoring of Valproic Acid Effects on Gene Expression Signatures in Adult Acute Myeloid Leukemia <i>Blood</i> , <b>2006</b> , 108, 2605-2605	2.2
41	Prognostic Impact of BAALC Expression in the Context of Other Molecular Markers in Cytogenetically Normal Acute Myeloid Leukemia <i>Blood</i> , <b>2007</b> , 110, 3485-3485	2.2
40	KIT Mutations Define Characteristic Gene Expression Signatures in Core Binding Factor Leukemias <i>Blood</i> , <b>2007</b> , 110, 3163-3163	2.2
39	Measurable Residual Disease (MRD) Monitoring in Acute Myeloid Leukemia (AML) with t(8;21)(q22;q22.1) RUNX1-RUNX1T1 Identifies Patients at High Risk of Relapse: Results of the AML Study Group (AMLSG). <i>Blood</i> , <b>2019</b> , 134, 2740-2740	2.2
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27	Distinct Expression Patterns in Cytogenetically Normal Acute Myeloid Leukemia (CN-AML) Characterized by Uniparental Disomy <i>Blood</i> , <b>2008</b> , 112, 1193-1193	2.2
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